VERSION WITH MARKINGS TO SHOW CHANGES MADE

In the title:

Please amend the title to read:

ARRAYS COMPRISING BACKGROUND FEATURES THAT PROVIDE FOR A MEASURE OF NON-SPECIFIC BINDING AND METHODS FOR USING THE SAME

In the claims:

50. (Amended) A hybridization assay comprising:

(a) contacting a sample of target nucleic acids under hybridization conditions ~~that require~~ where a target nucleic acid of 14 nucleotides in length ~~to have at least~~ must have no less than 70% sequence identity with a probe in order to hybridize to said probe with a collection of substrate bound probe nucleic acid features that includes at least one background nucleic acid feature that ~~minimally binds to its complementary target under said hybridization conditions~~ is an empirically observed inactive probe that does not hybridize to its fully complementary target as determined in an assay wherein said probe is provided in an array that is contacted with said fluorescently labeled fully complementary target under said hybridization conditions; and

(b) detecting the presence of target nucleic acids hybridized to said collection of probe nucleic acid features.

58. (Amended) A hybridization assay comprising:

(a) contacting a sample of target nucleic acids under hybridization conditions ~~that require~~ where a target nucleic acid of 14 nucleotides in length ~~to have at least~~ must have no less than 70% sequence identity with a probe in order to hybridize to said probe with a collection of substrate bound probe nucleic acid features that includes at least one

background nucleic acid feature, wherein said at least one background feature is made up of a probe nucleic acid selected from the group consisting of SEQ ID NOS: 05 to 32 ~~or a probe that similarly minimally binds to an R6G-labeled yeast cRNA target pool according to the test assay described in Example 3.B.~~; and

(b) detecting the presence of target nucleic acids hybridized to said collection of probe nucleic acid features.

59. (Amended) A hybridization assay comprising:

(a) contacting a sample of target nucleic acids under hybridization conditions ~~that require~~ where a target nucleic acid of 14 nucleotides in length ~~to have at least~~ must have no less than 70% sequence identity with a probe in order to hybridize to said probe with a collection of substrate bound probe nucleic acid features that includes at least one background nucleic acid feature, wherein said at least one background feature is made up of a probe nucleic acid that is chosen from: (i) a probe nucleic acid that forms a stable intramolecular structure; (ii) a probe nucleic acid that comprises reverse polarity nucleotide analogs; and (iii) a probe nucleic acid that comprises abasic phosphodiesters ~~minimally binds to an R6G-labeled yeast cRNA target pool according to the test assay described in Example 3.B.~~; and

(b) detecting the presence of target nucleic acids hybridized to said collection of probe nucleic acid features.

60. (Amended) A hybridization assay comprising:

(a) contacting a sample of detectably labeled target nucleic acids under hybridization conditions ~~that require~~ where a target nucleic acid of 14 nucleotides in length ~~to have at least~~ must have no less than 70% sequence identity with a probe in order to hybridize to said probe with an array of probe nucleic acid features that includes at least one background nucleic acid feature that ~~minimally binds to its complementary target under said hybridization conditions~~ is an empirically observed inactive probe that does not hybridize to its fully complementary target as determined in an assay wherein said probe is provided in an array that is contacted with said fluorescently labeled fully complementary target under said hybridization conditions;

(b) separating non-hybridized target nucleic acids from said array; and

(c) detecting the presence of target nucleic acids hybridized to said array probe

nucleic acid features.

62. (Amended) A hybridization assay comprising:

(a) contacting a sample of detectably labeled target nucleic acids conditions ~~that require~~ where a target nucleic acid of 14 nucleotides in length ~~to have at least~~ must have no less than 70% sequence identity with a probe in order to hybridize to said probe with an array of probe nucleic acid features that includes at least one background nucleic acid feature, wherein said at least one background feature is made up of a probe nucleic acid selected from the group consisting of SEQ ID NOS: 05 to 32 ~~or a probe that similarly minimally binds to an R6G-labeled yeast cRNA target pool according to the test assay described in Example 3.B.~~;

(b) separating non-hybridized target nucleic acids from said array; and

(c) detecting the presence of target nucleic acids hybridized to said array probe nucleic acid features.

63. (Amended) A hybridization assay comprising:

(a) contacting a sample of detectably labeled target nucleic acids conditions ~~that require~~ where a target nucleic acid of 14 nucleotides in length ~~to have at least~~ must have no less than 70% sequence identity with a probe in order to hybridize to said probe with an array of probe nucleic acid features that includes at least one background nucleic acid feature, wherein said at least one background feature is made up of a probe nucleic acid that is chosen from: (i) a probe nucleic acid that forms a stable intramolecular structure; (ii) a probe nucleic acid that comprises reverse polarity nucleotide analogs; and (iii) a probe nucleic acid that comprises abasic phosphodiesters ~~minimally binds to an R6G-labeled yeast cRNA target pool according to the test assay described in Example 3.B.~~;

(b) separating non-hybridized target nucleic acids from said array; and

(c) detecting the presence of target nucleic acids hybridized to said array probe nucleic acid features.

64. (Amended) A hybridization assay comprising:

(a) contacting a sample of target nucleic acids under hybridization conditions ~~that require~~ where a target nucleic acid of 14 nucleotides in length ~~to have at least~~ must have no less than 70% sequence identity with a probe in order to hybridize to said probe with an array of probe nucleic acid features that includes at least one background nucleic acid feature that

~~minimally binds to its complementary target under said hybridization conditions~~ is an empirically observed inactive probe that does not hybridize to its fully complementary target as determined in an assay wherein said probe is provided in an array that is contacted with said fluorescently labeled fully complementary target under said hybridization conditions;

(b) separating non-hybridized target nucleic acids from said array;

(c) detectably labeling target nucleic acids hybridized to said array of probe nucleic acid features; and

(d) detecting the presence of target nucleic acids hybridized to said array of probe nucleic acid features.

66. (Amended) A hybridization assay comprising:

(a) contacting a sample of target nucleic acids under hybridization conditions ~~that require~~ where a target nucleic acid of 14 nucleotides in length ~~to have at least~~ must have no less than 70% sequence identity with a probe in order to hybridize to said probe with an array of probe nucleic acid features that includes at least one background nucleic acid feature, wherein said at least one background feature is made up of a probe nucleic acid selected from the group consisting of SEQ ID NOS: 05 to 32 ~~or a probe that similarly minimally binds to an R6G-labeled yeast cRNA target pool according to the test assay described in Example 3.B.~~;

(b) separating non-hybridized target nucleic acids from said array;

(c) detectably labeling target nucleic acids hybridized to said array of probe nucleic acid features; and

(d) detecting the presence of target nucleic acids hybridized to said array of probe nucleic acid features.

67. (Amended) A hybridization assay comprising:

(a) contacting a sample of target nucleic acids under hybridization conditions ~~that require~~ where a target nucleic acid of 14 nucleotides in length ~~to have at least~~ must have no less than 70% sequence identity with a probe in order to hybridize to said probe with an array of probe nucleic acid features that includes at least one background nucleic acid feature, wherein said at least one background feature is made up of a probe nucleic acid that is chosen from: (i) a probe nucleic acid that forms a stable intramolecular structure; (ii) a probe nucleic acid that comprises reverse polarity nucleotide analogs; and (iii) a probe nucleic acid that comprises abasic phosphodiesters ~~minimally binds to an R6G-labeled yeast cRNA target~~

~~pool according to the test assay described in Example 3.B.~~;

(b) separating non-hybridized target nucleic acids from said array;

(c) detectably labeling target nucleic acids hybridized to said array of probe nucleic acid features; and

(d) detecting the presence of target nucleic acids hybridized to said array of probe nucleic acid features.

68. (Amended) A kit for use in a hybridization assay, said kit comprising:

a collection of substrate bound probe nucleic acid features that includes at least one background nucleic acid feature that is made up of a probe nucleic acid selected from the group consisting of SEQ ID NOS: 05 to 32 ~~minimally binds to its complementary target under hybridization conditions that require a target nucleic acid of 14 nucleotides in length to have at least 70% sequence identity with a probe in order to hybridize to said probe~~.

Cancel Claims 69 and 70.

71. (Amended) A hybridization assay comprising:

(a) contacting a sample of target nucleic acids under hybridization conditions ~~that require~~ where a target nucleic acid of 14 nucleotides in length ~~to have at least~~ must have no less than 70% sequence identity with a probe in order to hybridize to said probe with a collection of substrate bound probe nucleic acid features that includes at least one background nucleic acid feature made up of background probes that do not selectively bind to any of said target nucleic acids; and

(b) detecting the presence of target nucleic acids hybridized to said collection of probe nucleic acid features.

Please add the following new claims:

--79. (New) The method according to Claim 59, wherein said stable intramolecular structure is a hairpin.

80. (New) The method according to Claim 59, wherein said stable intramolecular structure is a pseudo-half knot.

81. (New) The method according to Claim 63, wherein said stable intramolecular structure is a hairpin.

82. (New) The method according to Claim 63, wherein said stable intramolecular structure is a pseudo-half knot.

83. (New) The method according to Claim 67, wherein said stable intramolecular structure is a hairpin.

84. (New) The method according to Claim 67, wherein said stable intramolecular structure is a pseudo-half knot.--